Remarks

Upon entry of the present amendment, claims 50-103 are pending. Claims 61, 63, 76, 88, 90, and 103 have been amended to correct improper grammar and integrate the Examiner's suggestions. The title was amended as suggested by the Examiner. Hence, no new matter has been introduced by these amendments.

Formal matters

a. The title was amended in accordance with the Examiner's requirement for a new title "that is clearly indicative of the invention to which the elected claims are drawn." *See,* Paper No. 10, page 2, second paragraph.

b. Applicants acknowledge the Examiner's comment regarding the polynucleotide and protein of the present invention being known by a different name in the published literature. *See*, Paper No. 10, page 2, third paragraph. Applicants are prepared to discuss the matter of re-naming the protein with the Examiner upon indication of allowable subject matter.

c. References AH-BX (Genbank accession numbers) of the Information Disclosure Statement filed on April 4, 2002 (Paper No. 9) were not considered because their relevance could allegedly not be assessed "in the absence of either a statement of relevance or an alignment to SEQ ID NO: 4", *See,* Paper No. 10, page 2, lines 15-18. Applicants respectfully disagree and traverse.

According to the M.P.E.P., section 609, pages 600-122, -123, a statement of relevance is required only if the cited references are not in the English language and is only encouraged if the references are lengthy and complex. Applicants assert that the references cited in the submitted Information Disclosure Statement do not meet any of those conditions and, therefore, such a statement is not required. Applicants respectfully request that the references AH-BX cited in the Information Disclosure Statement be considered and join a copy of the SB08-1449 submitted on April 4, 2002 to that effect.

Rejection under 35 U.S.C. § 101

Claims 50-103 were rejected under 35 U.S.C. § 101 as allegedly being "not supported by either a specific, substantial and credible asserted utility or a well established utility." *See,* Paper No. 10, page 2, last paragraph. Applicants respectfully disagree and traverse.

According to the M.P.E.P. § 2107.02, sub-sections III and IV, Applicants are entitled to a presumption of utility and it is the burden of the Office to establish a *prima facie* case of unpatentability and provide evidentiary support thereof. The PTO must accept the manner of making and using an invention disclosed in a specification "unless there is a reason for one of skill in the art to question the objective truth of the statement of utility or its scope." *In re Langer*, 183 U.S.P.Q. at 297; See also, *In re Marzocchi*, 58 C.C.P.A. 169 U.S.P.Q. 367, 369 (C.C.P.A. 1971) and *Utility Examination Guidelines*, 66 Fed. Reg. 1092, 1098-99 (Jan. 5, 2001). Indeed, the Federal Circuit recently articulated the standard for utility:

> The threshold of utility is not high: an invention is "useful" under section 101 if it is capable of providing some identifiable benefit. *See Brenner v. Manson*, 383 U.S. 519, 534 (1996); *Brooktree Corp. v. Advanced Micro Devices, Inc.*, 977 F.2d 1555, 1571 (Fed. Cir. 1992) ("To violate § 101 the claimed device must be totally incapable of achieving a useful result"); *Fuller v. Berger*, 120 F. 247, 275 (7th Cir. 1903) (the test for utility is whether the invention "is capable of serving any beneficial end").

Juicy Whip, Inc. v. Orange Bang Inc., 51 U.S.P.Q.2d 1700, 1702 (Fed. Cir. 1999).

Further, the burden is on the Examiner to establish why it is more likely than not that one of ordinary skill in the art would doubt (*i.e.*, "question") the truth of the statement of utility. *See,* M.P.E.P. § 2107.01(II)(A) at 2100-[31-32]. Thus, the Examiner must provide evidence sufficient to show that a person of ordinary skill in the art would consider the statement of asserted utility "false". *Id.* The Examiner must also present countervailing facts and reasoning sufficient to establish that a person of ordinary skill would not believe the applicants' assertion of utility. For the reasons set forth below, the burden that is necessary to establish and maintain a rejection for lack of utility under 35 U.S.C. § 101 has not been met.

As pointed out by the Examiner, on page 3 of Paper No. 10, the protein of the invention is described based on the isolated nucleotide sequence and by determination of structural homology with other Interleukins (*e.g.*, IL-17 and IL-20). *See*, for example, pages 14-16 of the

specification. Applicants are under no obligation to specifically disclose cellular or developmental expression patterns when such disclosure is not crucial to the claimed invention. However, Applicants point the Examiner to page 141 of the specification, where the tissue-specific expression of IL-22 is described.

As part of the rejection of claims 50-103 under 35 U.S.C. § 101, the Examiner asserts that function cannot be predicted based solely on structural similarity and cites some publications in support of this assertion, *See,* pages 5-6 of Paper No. 10. For instance, the Examiner asserts: "[F]urther, the relevant literature indicates that prediction of function from structure is not accurate, and reports examples of polypeptide families wherein individual members have distinct, and sometimes even opposite biological activities, such that the scattered similarities to other known interleukins cannot be taken to be predictive of any particular function."

Applicants respectfully disagree and traverse.

Applicants submit that the publications cited on pages 4 to 5 of Paper No. 10 are not germane to the IL-17 or IL-20 cytokine family to which the present claimed proteins belong. Simply because other unrelated superfamilies may contain a family member that does not exhibit the same activities as the rest of the protein family, does not indicate that IL-22 of the present invention cannot have similar biological functions as its homologs; *i.e.,* IL-17 or IL-20.

Applicants disclosed the claimed protein's homology to known a family of proteins involved in immunoregulation (*e.g.*, IL-17 and IL-20), and the tissue distribution determined for the claimed proteins (*See, e.g.,* page 141 of the specification). Therefore, it was determined that the claimed IL-22 would more likely than not be involved in immune system related disorders, such as, for example, those outlined on page 128 of the specification.

Also, simply because errors may occur in genome annotations does not indicate that the skilled artisan believes that the entire system of analysis is hopelessly flawed and would never use sequence similarity to assign function to a novel gene sequence. In fact, a careful consideration of the publications cited indicates that, contrary to the Examiner's contention that "the art acknowledges that function cannot be predicted solely on structural similarity to a protein found in the sequence databases", *See,* page 4 of Paper No. 10, the authors in the cited

papers all state that sequence databases are a powerful and useful tool in obtaining functional information for a novel gene sequence. Further, these authors all contend that it is the *automation* of functional annotation *without* further human analysis confirming the results that can propagate errors and may lead to mis-annotations of function.

For example, in Doerks *et al.*, TIG, vol. 14(6):248-250 (1998), the authors state on page 248 that:

> With the increasing amount of data, more and more software robots perform this task. While robots are the only solution to cope with the flood of data, they are also dangerous because they can currently introduce and propagate mis-annotation.

Nevertheless, these authors, on page 250, in the Summary section, assert "...we were able to provide some functional annotation for more than 700 of about 1300 proteins clustered in 25 of the 58 distinct UPFs...[t]his annotation is now being incorporated into PROSITE and SWISS-PROT so that these features can be assigned to newly sequenced genes as well." It appears that the authors are using the functional annotations obtained by the methods described therein, thus, they must have some confidence in the functional assignment.

The recognized shortcomings in automated annotation approaches are also at issue in Smith, T.F. & Zhang, X., Nature Biotechnology, Vol. 15:1222-1223 (1997). However, these authors also recognize that genomic annotations are a valid and successful tool. Specifically, the authors state on page 1222 that:

> This is, of course, a generalization of successful approaches used by many researchers to assign probable functions to new sequences when previously studied and recognizable homologs exist. However, when applied in an automated manner to large data sets with minimum review, such approaches can lead to serious degradation of the wealth of incoming genomic data.

In addition, the authors assert on page 1223 that:

> What must be done to avoid continued annotation inconsistency, incompleteness, and erroneous propagation? First, any automation must be rather sophisticated. It must, for a start, recognize large differences in the length of matching sequences; it must associate annotation with specific subsequences; it must recognize all differences among the annotations of the homologs to the matched sequence; and, wherever possible, sequence similarity should be identified via

shared conserved sequence patterns or profiles that have been carefully annotated, consistent with the entire family characterized by that pattern.

Clearly, the authors believe that automated annotations must be further reviewed by human analysis in order to more accurately assign functional annotations to new sequences. The authors do not state that function cannot be predicted based solely on sequence similarity, as alleged in the pending Office Action.

This sentiment is shared by Bork, Genome Research, Vol. 10:398-400 (2000). In Table 1 on page 399, Bork demonstrates how a prediction of functional features by homology is estimated to have a 90% accuracy, in spite of any limitations in its methods.

Bork in TIG, Vol.12 (10):425-427 (1996) again emphasizes that automated data handling and analysis can be a source of errors (*See,* pages 425 and 426). However, Bork explicitly states on page 427 that "although the list of problematic issues is much longer, we wish to point out that sequence databases are the most useful tool in sequence analysis and the question should be how can one further improve their value by enhancing the data storage, handling and retrieval?"

Similarly, Brenner, TIG, Vol. 15(4):132-133 (1999) on page 133, Table I demonstrates that the minimum error rate for the exemplified *M. genitalium* annotation ranges from 7-15%. Further, on page 132, Brenner states that "[t]o ensure that databases are kept usable, the intent of a gene annotation should be clear..." Therefore, Brenner does not dismiss the use of gene annotation as asserted by the Examiner.

Finally, in the last reference cited by the Examiner, Skolnick and Fetrow (Trends in Biotech, 18:34-39 (2000)) do not dismiss the use of sequence homology to determine a new protein's function. At page 36, right column, the authors state that "[F]or protein whose sequence identity is above ~30%, one can use homology modeling to build the structure." Once the structure is determined, one can apply a sequence-to-structure-to-function algorithm detailed in the article to infer the function of the unknown protein. The authors are targeting in their article "the 30-50% of protein whose function cannot be assigned by any current methods. (Conclusion, page 37)", a category into which the disclosed IL-22 does not fall.

On page 5 of Paper No. 10, it was alleged that, "the disclosed use for diagnosis, treatment or prevention of a disease cannot be considered to be specific or substantial, much less

credible, as there is no disclosure of any disease or condition which could be so diagnosed or treated."

Applicants respectfully disagree and traverse.

In the specification, there are listed several diseases and disorders for which IL-22 could be used in diagnostic or treatment methods, *See,* pages 128-134. Furthermore, Applicants describe the use of IL-22 in 'immunophenotyping' on page 99; immunophenotyping is as specific as the protein used to perform the assay and the fact that it is available for every single protein does not make it less relevant to the protein used in the assay. Furthermore, the disclosed IL-22 was characterized in the specification by expression pattern and by amino acid sequence homology; those characteristics classified it in the Interleukins superfamily. As opposed to the Examiner's affirmation, the combination of homology and expression pattern is accepted in the art as being predictive of function (as discussed above).

In view of the above explanations, Applicants respectfully submit that the present invention clearly demonstrates a specific, substantial, and credible asserted utility as disclosed in the specification. Accordingly, Applicants respectfully request that the rejection of claims 50-103 under 35 U.S.C. § 101, be reconsidered and withdrawn.

Rejection under 35 U.S.C. § 112, first paragraph

Claims 50-103 were rejected under 35 U.S.C. § 112, first paragraph, "since the claimed invention is not supported by either a specific, substantial and credible asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention." *See,* Paper No. 10, page 6, second paragraph.

Applicants respectfully disagree and traverse. For the reasons discussed above in response to the rejection under 35 U.S.C. § 101, Applicants submit that the claimed invention is supported by a specific, substantial, and credible utility. The Examiner "should not impose a 35 U.S.C. § 112, first paragraph, rejection grounded on a 'lack of utility' basis unless a 35 U.S.C. § 101 rejection is proper." M.P.E.P. § 2107(IV) at 2100-28 (Rev.1, Feb. 2000). Therefore, since the claimed invention complies with the utility requirement of 35 U.S.C. § 101, the rejection of

claims 50-103 under 35 U.S.C. § 112, first paragraph, based on lack of utility of the claimed invention, should be withdrawn.

Claims 77-103 were further rejected under 35 U.S.C. § 112, first paragraph "as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention." *See*, Paper No. 10, page 6, penultimate paragraph. In particular, the Examiner has requested that Applicants submit a statement regarding public availability of the deposit upon the granting of a patent. *Id*, last paragraph.

In compliance with the Examiner's request, Applicants provide herewith a statement indicating that all restrictions on availability of the deposited material to the public will be irrevocably removed upon the granting of a patent.

Claims 51, 67, and 77-103 were further rejected under 35 U.S.C. § 112, first paragraph "as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention." *See*, Paper No. 10, page 7, first paragraph. In particular, it was alleged that "claims 51, 67, 78, and 94 are not supported by the specification because there is no description of any glycosylation of the protein represented by SEQ ID NO: 4 residues 1-160." *Id.*, page 7, second paragraph. Applicants respectfully disagree and traverse.

At page 4, lines 9-12 of the specification, it is stated that,

> "[F]igures 2A and 2B show the nucleotide sequence (SEQ ID NO: 3) and the deduced amino acid sequence (SEQ ID NO: 4) of IL-22. The locations of conserved Domains I-IV (see below) are underlined and labeled as such. The locations of two potential N-linked glycosylation sites are identified by a bolded asparagine symbol (N) accompanied by a bolded pound sign (#) located above the initial nucleotide of the codon encoding the corresponding asparagine. "

(emphasis added).

Furthermore, at page 6, lines 20-24 of the specification, it is also stated that,

> "[F]igure 8 shows the nucleotide sequence (SEQ ID NO: 31) and the deduced amino acid sequence (SEQ ID NO: 32) of an IL-22. The locations of conserved Domains I-IV and VI-VII are underlined and labeled as such. The locations of two potential N-linked glycosylation sites are identified by a bolded asparagine symbol (N) accompanied by a bolded pound sign (#) located above the initial nucleotide of the codon encoding the corresponding asparagine. The two potential N-linked glycosylation sites are located at Asn-39 (N-39, A-40, S-41) and Asn-152 (N-152, S-153, S-154) of SEQ ID NO: 32."

(emphasis added).

The determination of potential glycosylation sites on a polypeptide of known sequence is well known in the art and highly predictable. It is also well known in the art that the choice of a heterologous expression system for a given sequence will affect the post-translational modifications on the expressed polypeptide, *See, e.g.,* specification at page 91, lines 15-18, such as glycosylation. Furthermore, given the teachings of the present specification, one of ordinary skill in the art would be readily able to produce and generate antibodies to glycosylated forms of IL-22 protein. Stated otherwise, the disclosure of the present application and state of the art at the time of filing would permit one of ordinary skill in the art to generate antibodies to glycosylated forms of IL-22 protein. Therefore, Applicants have provided ample support for the claims targeted to antibodies binding to glycosylated proteins.

It was also alleged that "[w]ith the exception of the unmodified protein of SEQ ID NO: 4, the skilled artisan cannot envision the detailed chemical structure of the glycosylated protein, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation." *See*, Paper No. 10, page 7, last paragraph.

Applicants respectfully disagree and traverse.

A rejection because "a conception is not achieved until reduction to practice has occurred" is neither supported by the U.S.P.T.O. nor by case law. As stated in the Revised Written Description Guidelines (Fed. Reg. Vol. 66, No. 4, Section 1, page 1104, Friday January 2, 2001, emphasis added):

> To satisfy the written description requirement, a patent specification must describe the claimed invention in sufficient detail that one skilled in the art can reasonably conclude that the inventor had possession of the claimed invention by describing the claimed invention with all its limitations using such descriptive means as words, structures, figures, diagrams, and formulas that fully set forth the claimed invention. Possession may be shown *in a variety of ways* including description of a reduction to practice, *or* by showing that the invention was "ready for patenting" such as by the disclosure of drawings or structural chemical formulas that show that the invention was complete, *or* by describing *distinguishing characteristics* sufficient to show that the applicants was in possession of the claimed invention.

Therefore, *requiring* a reduction to practice to show conception as the *only* way to satisfy written description is incorrect by the U.S.P.T.O.'s own guidelines. Such a requirement also flies in the face of the underlying principles of filing a patent application; it in effect nullifies the practice of a constructive reduction to practice (*e.g.*, filing a patent application) and placing the public on early notice of the subject matter in the application. This cannot be the purpose of the Written Description Guidelines.

Furthermore, the M.P.E.P. instructs:

> An adequate written description of the invention may be shown by any description of sufficient, relevant, identifying characteristics so long as a person skilled in the art would recognize that the inventor had possession of the claimed invention. *See, e.g., Purdue Pharma L.P. v. Faulding Inc.*, 230 F.ed 1320, 1323, 56 USPQ2d 1481, 1483 (Fed. Cir. 2000)....

M.P.E.P., 8th Edition, § 2163 II(A)(3)(a) (August 2001).

The M.P.E.P. further clarifies:

> What is conventional or well known to one of ordinary skill in the art need not be disclosed in detail. *See, Hybritech Inc. v. Monoclonal Antibodies, Inc.*, 802 F.2d at 1384, 231 USPQ at 94. If a skilled artisan would have understood the inventor to be in possession of the claimed invention at the time of filing, even if every nuance of the claims is not explicitly described in the specification, the adequate description requirement is met. *See, e.g., Vas-Cath*, 935 F.2d at 1563, 19 USPQ2d at 1116; *Martin v. Johnson*, 454 F.2d 746, 751, 172 USPQ 391, 395 (CCPA 1972) (stating "the description need not be in *ipsis verbis* [*i.e.*, "in the same words"] to be sufficient").

Id.

And, when the present application was filed, it was well known by those of ordinary skill in the art that expression of recombinant proteins in different cell types produces proteins with varied patterns of post-translational glycosylation. For example, expression of recombinant proteins in *E. coli* was known to produce proteins without post-translational glycosylation, whereas expression in insect cells was known to produce proteins with relatively simple patterns of glycosylation, and expression in mammalian or human cells was known to produce proteins with highly complex patterns of post-translational glycosylation. Indeed, in addition to the specifics of N-linked glycosylation discussed above, the present specification also taught that depending upon the host employed (*e.g.*, bacterial, yeast, higher plant, insect, or mammalian cells), recombinantly produced IL-22 polypeptides may be glycosylated or may be non-glycosylated. *See, e.g.*, specification at page 92, lines 15-28; and, page 109, lines 11-18. Moreover, armed with the teachings in the present specification, one of ordinary skill in the art would have been able to generate antibodies, without undue experimentation, to variously glycosylated forms of the novel IL-22 protein, simply by isolating the protein from the appropriate cell type (*e.g.*, bacterial, yeast, higher plant, insect, or mammalian cell) and immunizing an appropriate animal (*e.g.*, mouse, rabbit, horse, goat).

Furthermore, in basing the current claims rejection on a premise that "the skilled artisan cannot envision the detailed chemical structure of the glycosylated protein," the Examiner is imposing a higher standard than is even suggested by the PTO training guidelines. For example, these guidelines teach "[I]t is also well known that antibodies can be made against virtually any protein." *See, Example 16: Antibodies*, Revised Interim Written Description Guidelines Training Materials, at http://www.uspto.gov/web/menu/written.pdf. However, if the Examiner's current written description standard were applied, Applicants would be required to present protein crystal structures (so that the skilled artisan could "envision the detailed chemical structure") before antibody claims "against virtually any protein" could be allowed.

Applicants respectfully request that the rejection of claims 51, 67, and 77-103 under 35 U.S.C. § 112, first paragraph be reconsidered and withdrawn.

Claims 77-103 were also rejected under 35 U.S.C. § 112, first paragraph, based on the allegation that "'[A]ll or most' is not an adequate written description of the deposited material." *See*, Paper No. 10, page 8, second paragraph. Applicants respectfully disagree and traverse.

In *Enzo Biochem, Inc., v. Gen-Probe Incorporated*, 2002 U.S. App. LEXIS 14328 (July 15, 2002), the Federal Circuit held that "reference in the specification to a public depository, which makes its contents accessible to the public when it is not otherwise accessible in written form, constitutes an adequate description of the deposited material sufficient to comply with the written description requirement of § 112, P1." Applicants assert that the deposit indicated at page 9, lines 7-10 of the specification regarding SEQ ID NO: 3 is sufficient to comply with the written requirement of 35 U.S.C. § 112, first paragraph.

In view of the above explanation, Applicants respectfully request that the rejection of claims 77-103 under 35 U.S.C. § 112, first paragraph be reconsidered and withdrawn.

Rejection under 35 U.S.C. § 112, second paragraph

Claims 51, 57, 58, 63-65, 67, 72, 73, 78, 84, 85, 90-92, and 94-103 were rejected under 35 U.S.C. § 112, second paragraph "as being indefinite for failing to point out and distinctly claim the subject matter which applicant regards as the invention." *See*, Paper No. 10, page 8, lines 16-18. In particular, claims 51, 67, 78, and 94 were rejected "because it is not clear how the glycosylation state of the protein affects the claimed antibodies". *See,* Paper No. 10, page 8, lines 19-22. In view of the explanations provided above, Applicants respectfully submit that they have addressed the Examiner's concerns regarding the glycosylation of IL-22 and respectfully request that the rejection of claims 51, 57, 58, 63-65, 67, 72, 73, 78, 84, 85, 90-92, and 94-103 under 35 U.S.C. § 112, second paragraph be reconsidered and withdrawn.

Claims 57, 58, 72, 73, 84, 85, 99, and 100 were rejected "as it is not clear how the recitation that the antibody can be used in a particular assay further limits the claimed antibody." *See,* Paper No. 10, page 8, lines 23-26.

Applicants herein offer clarification. It is well known in the art that, in a Western blot, the antibody binds to a denatured form of the protein. By contrast, in an ELISA assay, the antibody binds to a non-denatured form of the protein. Therefore, the recitation that the antibody can be used in a particular assay does further limit the claimed antibody and does not render the claims indefinite.

Applicants respectfully request that the rejection of claims 57, 58, 72, 73, 84, 85, 99, and 100 under 35 U.S.C. § 112, second paragraph be reconsidered and withdrawn.

Claims 63 and 90 were rejected as being grammatically incorrect, *See,* Paper No. 10, page 8, line 27 to page 9, line 3.

Claims 63 and 90 have been amended herein according to the Examiner's suggestions. Applicants respectfully request that the rejection of claims 63 and 90 35 U.S.C. § 112, second paragraph be reconsidered and withdrawn.

Claims 61, 62, 76, 88-89, and 103 were rejected as being incomplete, *See,* Paper No. 10, page 9, lines 4-9.

Claims 61, 62, 76, 88-89, and 103 have been amended herein according to the Examiner's suggestions. Applicants respectfully request that the rejection of claims 61, 62, 76, 88-89, and 103 under 35 U.S.C. § 112, second paragraph be reconsidered and withdrawn.

Rejection under 35 U.S.C. § 102(b)

Claims 50, 51, 53-58, 61-65, 67, 77, 78, 80-85, 88, 89, 90, 92, 94, 96-100, and 103 were rejected under 35 U.S.C. § 102(b) as being anticipated by Sutcliffe (U.S. Patent No. 5,242,798, later referred to as "Sutcliffe"), *See,* Paper No. 10, page 9. Applicants respectfully disagree and traverse.

Regarding the rejection of claims under 35 U.S.C. § 102(b), the M.P.E.P states that:

> "[A] claim is anticipated only if each and every element as set forth in the claim is found, either expressly or inherently described, in a single prior art reference." *Verdegaal Bos. V. Union Oil Co. of California*, 814 F.2d 628, 631, 2 USPQD2d 1051, 1053 (Fed. Cir. 1987). "The identical invention must be shown in as complete detail as is contained in the ... claim." *Richardson v. Suzuki Motor Co.*, 868 F.2d 1226, 1236, 9 USPQD2d 1913, 1920 (Fed. Cir. 1989).

M.P.E.P., 8th Edition, § 2131 (August 2001).

As stated in Paper No. 10, page 9, lines 21-22, Sutcliffe discloses a synthetic peptide P2 having 13 amino acids, among which 6 match SEQ ID NO: 4. However, even if antibodies raised against the P2 peptide of Sutcliffe would bind a mere 6 amino acid region shared in common with IL-22, such antibodies are not encompassed by the present claims. The present claims encompass antibodies that specifically bind to a protein of sequence SEQ ID NO: 4, or the polypeptide encoded by the cDNA in ATCC Deposit No. 209665. Hence, antibodies that bind to both the P2 peptide and polypeptides of the present invention are not encompassed by the pending claims. Furthermore, it is stated in the Office Action that "[T]he claims differ from those rejected under 35 U.S.C. § 102(b) above in that they recite that the antibody is a monoclonal antibody, or that the claimed matter is a cell or hybridoma that produces such an antibody." *See*, Paper No. 10, page 11, first full paragraph. Hence, the reference cited in the rejection does not teach each and every element of the disclosed invention.

In view of these arguments, Applicants respectfully request that the rejection of claims 50, 51, 53-58, 61-65, 67, 77, 78, 80-85, 88, 89, 90, 92, 94, 96-100, and 103 under 35 U.S.C. § 102(b) be withdrawn.

Rejection under 35 U.S.C. § 103(a)

Claims 50, 60, 66-67, 69-76, 86, 87, 91, 93, 101, and 102 were rejected under 35 U.S.C. § 103(a) as being unpatentable over Sutcliffe (*See,* above), in view of Coughlin (U.S. Patent No. 5,256,766, later referred to as "Coughlin"). *See*, Paper No. 10, page 10. Applicants respectfully disagree and traverse.

In order for a rejection under 35 U.S.C. § 103(a) to be valid, three criteria must be met (*See,* M.P.E.P. 706.02(j)):

a) there must be some suggestions or motivation to modify or to combine reference teachings;

b) there must be a reasonable expectation of success; and

c) the prior art reference (or references when combined) must teach or suggest all the claim limitations

(emphasis added).

As discussed above, Sutcliffe does not disclose the present invention and therefore there would be no motivation or suggestion to use Sutcliffe's teachings, alone or in combination with any other reference, to obtain the present invention. Considering that the antibodies against the P2 peptide of Sutcliffe are not encompassed by the present claims, there would have been no motivation to isolate or prepare monoclonal antibodies or hybridoma or cell producing said antibodies. Accordingly, Applicants respectfully request that the rejection of claims 50, 60, 66-67, 69-76, 86, 87, 91, 93, 101, and 102 under 35 U.S.C. § 103(a) be withdrawn.

Claims 50-103 were rejected under 35 U.S.C. § 103(a) as being unpatentable over Bonaldo *et al.* (1993, locus HUMNOTIA), in view of Sibson (WO94/01548). *See*, Paper No. 10, page 11. Applicants respectfully traverse.

The Bonaldo reference is a single, non-explicit sequence from a human chromosome specific mRNA for which no open reading frame is disclosed or suggested, no encoded polypeptide is disclosed or suggested, no polypeptide function or activity is disclosed or suggested. The fact that it is "generally useful", as stated on page 11, line 22 of Paper No. 10, to place a desired cDNA sequence into an expression vector is not enough of a motivation to realize the presently claimed antibodies. Further, there would have been no reasonable expectation of success using the disclosed Bonaldo's sequence as no standard features, such as an open reading frame, are not disclosed nor evident from the HUMNOTIA sequence. As such, the combination of Bonaldo in view of Sibson does not teach or suggest any, much less all the present claim limitations of the invention. Therefore, the present invention is not obvious over the combination of references of the prior art. Applicants therefore respectfully request that the rejection of claims 50-103 under 35 U.S.C. § 103(a) be withdrawn.

Conclusion

Applicants respectfully request that the above-made amendments and remarks be entered and made of record in the file history of the instant application. If there are any fees due in connection with the filing of this paper, please charge the fees to our Deposit Account No. 08-3425. If a fee is required for an extension of time under 37 C.F.R. § 1.136 not accounted for

above, such an extension is requested and the fee should also be charged to our Deposit Account.

Dated: October 10, 2002

Respectfully submitted,

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VIA HAND DELIVERY OCTOBER 10, 2002

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:
Ebner et al.

Docket No.: PF470P1

Application No.: 09/731,816

Group Art Unit: 1647

Filed: December 8, 2000

Examiner: L. Spector

For: INTERLEUKIN-22 ANTIBODIES

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Title:

INTERLEUKIN-[~~21 and~~] 22 **ANTIBODIES**

In the Claims:

61. A method of detecting IL-22 protein in a biological sample comprising:
(a) contacting the biological sample with the antibody or fragment thereof of claim 50 **to create a complex with IL-22 protein;** [~~,~~] and
(b) detecting **said complex** [~~the IL-22 protein~~] in the biological sample.

63. An isolated antibody [~~or fragment thereof~~] obtained from an animal that has been immunized by a protein consisting of amino acid sequence 1 to 160 of SEQ ID NO:4, **or a fragment of said antibody**, wherein said antibody or fragment thereof specifically binds to said amino acid sequence.

76. A method of detecting IL-22 protein in a biological sample comprising:
(a) contacting the biological sample with the antibody or fragment thereof of claim 66 **to create a complex with IL-22 protein**; and
(b) detecting **said complex** [~~the IL-22 protein~~] in the biological sample.

88. A method of detecting IL-22 protein in a biological sample comprising:

(a) contacting the biological sample with the antibody or fragment thereof of claim 77 **to create a complex with IL-22 protein;** [,] and

(b) detecting **said complex** [~~the IL-22 protein~~] in the biological sample.

90. An isolated antibody [~~or fragment thereof~~] obtained from an animal that has been immunized with a protein consisting of the amino acid sequence of the complete polypeptide encoded by the cDNA contained in ATCC Deposit Number 209665, **or a fragment of said antibody**, wherein said antibody or fragment thereof specifically binds to said amino acid sequence.

103. A method of detecting IL-22 protein in a biological sample comprising:

(a) contacting the biological sample with the antibody or fragment thereof of claim 90 **to create a complex with IL-22 protein**; and

(b) detecting **said complex** [~~the IL-22 protein~~] in the biological sample.